SEQUENCE LISTING

<110> SYNGENTA PARTICIPATIONS AG

<120> EXPRESSION IN PLANTS OF ANTIBODIES AGAINST ENTEROTOXIGENIC ESCHERICHIA COLI

<130> S 70235/WO

<150> US 60/448429

<151> 2003-02-18

<160> 80

<170> PatentIn version 3.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K99 codon optimised VH

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actagtgagg tgcagctcgt ggagtccggc ggcggcttcg tgaagccggg cggctccctc 60

aagctctcct gcgccgcctc cggcttcacc ttctccgact acttcatgtc ctggattcgc 120

cagaccccgg agaagcgcct ggagtgggtc gccaccatca acaacggcgg ctcccacacc 180

tactgctccg acaacgtgaa gggccgcttc accaccttcc gcgacaacgt gaagaacacc 240

ctctacctcc agatgtcctc cctcaacttc gaggacaccg ccatgtacta ctgcgcccgc 300

gcctactacc gcttcgacgt gcgcgcctgg ttctcctact ggggccaggg caccctcgtg 360

accgtgtcca cggccaagac caccccgccg tccgtctac 399

<210> 2

<211> 582

<212> DNA

<213> Artificial Sequence

<220>

<223> anti K99 Codon optimised VL

<400> 2
agtgacatcc tcctcaccca gtccccggcc atcctctcca tgatcccgcg ccagcgcgtg 60

tccttctcct gccgcgcctc ccagatcatc ggcaccacca tccactggtc ccagcagcgc 120

accgacggct ccccgcgcct cctcatccag tgcgcctccg agtccatctc cggcatcccg 180

tcccgcttct ccggcaccgg ctccggcacc gacttcaccc tcaacttcaa ctccgtggag 240

tccgagtaca tcaccgacta ctactgccag cagtccaaca cctggccgac ctacccgttc 300

ggcggcggca ccaagctcga gatcaagcgc gccgacgccg ccccgaccgt gtccatcttc 360

ccgccgtcct ccgagcagct cacctccggc ggcgcgtccg tggtgtgctt cctcaacaac 420

ttctacccga aggacatcaa cgtgaagtgg aagatcgacg gctccgagcg ccagaacggc 480

gtgctcaact cctggaccga ccaggactcc aaggactcca cctactccat gtcctccacc 540

ctcaccctca ccaaggacga gtacgagcgc cacaactcct ac 582

<210> 3

<211> 399

<212> DNA

<213> Mouse

<400> 3
actagtgaag tgcaactggt ggagtctggg ggaggcttcg tgaagcctgg agggtccctg 60

aaactctcct gtgcagcctc tggattcact ttcagtgact atttcatgtc ttggattcgc 120

cagactccgg aaaagaggct ggagtgggtc gcaaccatta ataatggtgg tagtcacacc 180

tactgttcag acaatgtgaa gggacgattt acaactttca gagacaatgt caaaaacacc 240

ctgtaccttc aaatgagcag tctgaacttt gaggacacag ccatgtatta ctgtgcaaga 300

gcctactata ggttcgacgt gagggcctgg ttttcttatt ggggccaagg gactctggtc 360

actgtctcta cagccaaaac gacaccccca tctgtctac 399

<210> 4

<211> 330

<212> DNA

<213> Mouse

<400> 4
actagtgaca tcttgctgac tcagtctcca gccatcctgt ctatgattcc aagacaaaga 60

gtcagtttct cctgcagggc cagtcagatc attggcacaa ccatacactg gtctcagcaa 120

agaacagatg gttctcctag gcttctcata cagtgtgctt ctgagtctat ctctgggatc 180

ccttccaggt ttagtggcac tggatcaggg acagatttta ctcttaactt caacagtgtg 240

gagtctgaat atattacaga ttattactgt caacaaagta atacctggcc aacgtacccg 300

ttcggagggg ggaccaagct cgagataaaa 330

<210> 5

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VH from 17_44

<400> 5
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aagctctcct gcgccgcctc cggcttcacc ttctcctcct tcgccatgca ctgggtgcgc 120

caggccccag agaagggcct ggagtgggtg gcctacatct cctccggctc catcaccatc 180

tactacgccg acaccgtgaa gggccgcttc accgtgtccc gcgacaaccc gaagtccacc 240

ctcttcctcc agatgacctc cctccgcagc gaggacaccg ccatgtacta ctgcgcccgc 300

gacgactacg gctcctccgg ctggtacttc gacgtctggg gcgctggcac cacggtgacc 360

gtgtcctcgg ccaagaccac cccgccgtcc gtctac 396

<210> 6

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VL from 17_44

<400> 6
actagtgaca tcgtgatgtc ccagtccccg tcctccctcg ccgtgtccgc tggcgagaag 60

gtcaccatgt cctgcaagtc ctcccagtcc ctcctcaact cccgcacccg caagaactac 120

ctcgcctggt atcagcagaa gccgggccag tccccgaagc tcctcatcta ctgggcctcc 180

acccgcgagt ccggcgtgcc ggaccgcttc accggctccg gctccggcac cgacttcacc 240

ctcaccatct cctccgtgca ggcggaggac ctcgccgtgt actactgcac ccagtcctac 300

aacctcctca ccttcggcgc cggtaccaag ctcgag 336

<210> 7

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VH from 36_41

<400> 7
actagtgagg tccagctgca gcagtctgga cctgaactag tgaagactgg ggcttcagtg 60

aagatatcct gcaaggcttc tgattactca ctcactgatt actacatgca ctgggtcaag 120

cagagccatg gagagagcct tgagtggatt ggatatatta atttttacaa tggtgctact 180

aactacaacc agaagttcaa gggcaaggcc acatttactg tagacacatc ctccagcaca 240

gtctacatgc agttcaacag cctgacatct gaagactctg cggtctatta ttgtgtaaga 300

gaagcattac tacggaacta tgctatggac tactggggtc aaggaacctc agtcaccgtc 360

tcctcagcca aaacgacacc cccatctgtc tac 393

<210> 8

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VL from 36_41

<400> 8
actagtgaaa atgtgctcac ccagtctcca gcaatcatgt ctgcatctcc aggggaaaag 60

gtcaccatga cctgcagggc cagctcaagt gtaagttccc gttacttgca ctggtaccag 120

cagaagtcag gtgcctcccc caaactctgg atttatagca catccaactt ggcttctgga 180

gtccctgctc gcttcagtgg cagtgggtct gggacctctt actctctcac aatcagcagt 240

gtggaggctg aagatgctgc cacttattac tgccagcaat acagtggtta cccgtggacg 300

ttcggtggag gcaccaagct cgag 324

<210> 9

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VH from 7_46

<400> 9
actagtgaag tgaagcttga ggagtctgga ggaggcttgg tgcaacctgg aggatccatg 60

agactctcct gtgttgcctc tggattcact ttcagtaact actggatgaa ctgggtccgc 120

cagtctccag agaaggggct tgagtgggtt gctgaaatta gattgacatc taataatttt 180

gcaacacatt atgcggagtc tgtgaaaggg aggttcacca tctcaagaga tgattccaaa 240

agtagtgtct acctgcaaat gaacaactta agagctgaag acactggcat ttattactgt 300

accaggcctt actacggtgg taggttcttc tactggtact tcgatgtctg gggcgcaggg 360

accacggtca ccgtctcctc aaccaaaacg acacccccat ctgtctac 408

<210> 10

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VL from 7_46

<400> 10
actagtgaaa ttgtgctcac ccagtctcca accaccatgg ctgcatctcc cggggagaag 60

atcactatca cctgcagtgc cagctcaagt ataagttcca attacttgca ttggtatcag 120

cagaagccag gattctcccc taaactcttg atttatagga catccaatct ggcttctgga 180

gtcccagttc gcttcagtgg cagtgggtct gggacctctt actctctcac aattggcacc 240

atggaggctg aagatgttgc cacttactac tgccagcagg gtaatagtat accattcacg 300

ttcggctcgg ggacaaagct cgag 324

<210> 11

<211> 363

<212> DNA

<213> Mouse

<400> 11

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tcctgtgcag cctctggatt cactttcagt agctttgcaa tgcactgggt tcgtcaggct 120

ccagagaagg ggctggagtg ggtcgcatat attagtagtg gcagtattac catctactat 180

gcagacacag tgaagggccg attcaccgtc tccagagaca atcccaagag caccctgttc 240

ctgcaaatga ccagtctaag gtctgaggac acggccatgt attactgtgc aagagacgac 300

tacggtagta gcgggtggta cttcgatgtc tggggcgcag ggaccacggt caccgtctcc 360

tca 363

<210> 12

<211> 350

<212> DNA

<213> Mouse

<400> 12

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atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cacyctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcacgcaatc ttataatctg 300

ctcacgttcg gtgctgggac caagctggaa ctgaatcggg ctgatgctgc 350

<210> 13

<211> 410

<212> DNA

<213> Mouse

<400> 13
gaggtccagc tgcagcagtc tggacctgaa ctagtgaaga ctggggcttc agtgaagata 60

tcctgcaagg cttctgatta ctcactcact gattactaca tgcactgggt caagcagagc 120

catggagaga gccttgagtg gattggatat attaattttt acaatggtgc tactaactac 180

aaccagaagt tcaagggcaa ggccacattt actgtagaca catcctccag cacagtctac 240

atgcagttca acagcctgac atctgaagac tctgcggtct attattgtgt aagagaagca 300

ttactacgga actatgctat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360

gccaaaacga caccccatc tgtctatcca ctggccccta ctagtgctgc 410

<210> 14

<211> 317

<212> DNA

<213> Mouse

<400> 14
gaaaatgtgc tcacccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 60

atgacctgca gggccagctc aagtgtaagt tcccgttact tgcactggta ccagcagaag 120

tcaggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtccct 180

gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagtgtggag 240

gctgaagatg ctgccactta ttactgccag caatacagtg gttacccgtg gacgttcggt 300

ggaggcacca agctgga 317

<210> 15

<211> 374

<212> DNA

<213> Mouse

<400> 15
gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgagactc 60

tcctgtgttg cctctggatt cactttcagt aactactgga tgaactgggt ccgccagtct 120

ccagagaagg ggcttgagtg ggttgctgaa attagattga catctaataa ttttgcaaca 180

cattatgcgg agtctgtgaa agggaggttc accatctcaa gagatgattc caaaagtagt 240

gtctacctgc aaatgaacaa cttaagagct gaagacactg gcatttatta ctgtaccagg 300

ccttactacg gtggtaggtt cttctactgg tacttcgatg tctggggcgc agggaccacg 360

gtcaccgtct cctc 374

<210> 16

<211> 318

<212> DNA

<213> Mouse

<400> 16

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atcacctgca gtgccagctc aagtataagt tccaattact tgcattggta tcagcagaag 120

ccaggattct cccctaaact cttgatttat aggacatcca atctggcttc tggagtccca 180

gttcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaattgg caccatggag 240

gctgaagatg ttgccactta ctactgccag cagggtaata gtataccatt cacgttcggc 300

tcggggacaa agctcgag 318

<210> 17

<211> 134

<212> PRT

<213> Artificial Sequence

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<223> anti-k99 heavy chain variable region

<400> 17

Ala Thr Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Phe Val Lys
1 5 10 15

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

Ser Asp Tyr Phe Met Ser Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu
35 40 45

Glu Trp Val Ala Thr Ile Asn Asn Gly Gly Ser His Thr Tyr Cys Ser
50 55 60

Asp Asn Val Lys Gly Arg Phe Thr Thr Phe Arg Asp Asn Val Lys Asn
65 70 75 80

Thr Leu Tyr Leu Gln Met Ser Ser Leu Asn Phe Glu Asp Thr Ala Met
85 90 95

Tyr Tyr Cys Ala Arg Ala Tyr Tyr Arg Phe Asp Val Arg Ala Trp Phe
100 105 110

Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr Ala Lys Thr
115 120 125

Thr Pro Pro Ser Val Tyr
130

<210> 18

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-k99 light chain

<220>

<221> MISC_FEATURE

<222> (225)..(226)

<223> X at positions 225 and 226 designates an unknown amino acid

<400> 18

Ala Thr Ser Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Met
1 5 10 15

Ile Pro Arg Gln Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ile Ile
20 25 30

Gly Thr Thr Ile His Trp Ser Gln Gln Arg Thr Asp Gly Ser Pro Arg
35 40 45

Leu Leu Ile Gln Cys Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg
50 55 60

Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Asn Phe Asn Ser
65 70 75 80

Val Glu Ser Glu Tyr Ile Thr Asp Tyr Tyr Cys Gln Gln Ser Asn Thr
85 90 95

Trp Pro Thr Tyr Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
210 215 220

Xaa Xaa Thr Gly Phe
225

<210> 19

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT2

<400> 19
accatggatt ttcaagtgca gattttcag 29

<210> 20

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT3

<400> 20
caccatggag wcacakwctc agtgtctttr t 31

<210> 21

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT4

<400> 21
caccatgkcc ccwrctcagy tyctkgt 27

<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT5

<400> 22
caccatgaag ttgcctgtta ggctgttg 28

<210> 23

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MH1

<400> 23
atatccacca tggratgsag ctgkgtmats ctctt 35

<210> 24

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MH2

<400> 24
atatccacca tgracttcgg gytgagctkg gtttt 35

<210> 25

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 33615

<400> 25
gaagatctag acttactatg cagcatcagc 30

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MVG1R

<400> 26
ggcagcacta gtaggggcca gtggata 27

<210> 27

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MVG2R

<400> 27
gaggarccac tagtatctcc acacmcaggg gccag 35

<210> 28

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> ER transit peptide

<400> 28

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser

<210> 29

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 29
acgcgtcgat catccaggtg caac 24

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30
actagtggcg ctcgcagcga ga 22

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31
accggttctg ttctgcacaa agtgt 25

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 32
acgcgtttgt acccctggat t 21

<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 33
acgcgtttgc atgcctgcag tg 22

<210> 34

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 34
agtccaacgg tggagcggaa ct 22

<210> 35

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> ER retention signal

<400> 35

Ser Glu Lys Asp Glu Leu
1 5

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 36
agcttggatc cactagtacc ggtacgcgtg 30

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 37
aattcacgcg taccggtact agtggatcca 30

<210> 38

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 38
catgtgaggc cacccacaag acctccacct ccccaatcgt gaagagcttc aaccgcaacg 60

agtgctgata ga 72

<210> 39

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 39
ccggtctatc agcactcgtt gcggttgaag ctcttcacga ttggggaggt ggaggtcttg 60

tgggtggcct ca 72

<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 40
agcttacgcg tggatccact agtgagctcg gtaccg 36

<210> 41

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 41
aattcggtac cgagctcact agtggatcca cgcgta 36

<210> 42

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 42
ccgggcaagt ccgagaagga cgagctgtga taggagctca aggtaccgaa ttca 54

<210> 43

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 43
agcttgaatt cggtaccttg agctcctatc acagctcgtc cttctcggac ttgc 54

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer IIA

<400> 44
aagcagtggt atcaacgcag agt 23

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer SMART IIA

<400> 45
aagcagtggt atcaacgcag agtacgcggg 30

<210> 46

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K99HC-3'

<400> 46
aagtagacag atgggggtgt cg 22

<210> 47

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_746_VAR_H5'

<400> 47
gccactagtg aagtgaagct tgaggag 27

<210> 48

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_1744_VAR_H5'

<400> 48
gccactagtg atgtgcagct ggtgga 26

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_3641_VAR_H5'

<400> 49
gccactagtg aggtccagct gcagcag 27

<210> 50

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_746_VAR_L5

<400> 50
ccactagtga aattgtgctc acccag 26

<210> 51

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_746_VAR_L3

<400> 51
ttatctcgag ctttgtcccc gagccgaa 28

<210> 52

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_3641_VAR_L5

<400> 52
gccactagtg aaaatgtgct cacccag 27

<210> 53

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_3641_VAR_L3

<400> 53
ttatctcgag cttggtgcct ccaccgaa 28

<210> 54

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_1744_VAR_L5

<400> 54
gccactagtg acattgtgat gtcacag 27

<210> 55

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_1744_VAR_L3

<400> 55
ttatctcgag cttggtccca gcaccgaacg 30

<210> 56

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain Variable Domain Motif

<400> 56

Lys Leu Glu Ile Lys
1 5

<210> 57

<211> 972

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus nucleotide sequence of murine IgG1 Heavy Chain

<400> 57
gccaaaacga cacccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac 60

tccatggtga ccctgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc 120

tggaactctg gatccctgtc cagcggtgtg cacaccttcc cagctgtcct gcagtctgac 180

ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 240

acctgcaacg ttgcccaccc ggccagcagc accaaggtgg acaagaaaat tgtgcccagg 300

gattgtggtt gtaagccttg catatgtaca gtcccagaag tatcatctgt cttcatcttc 360

cccccaaagc ccaaggatgt gctcaccatt actctgactc ctaaggtcac gtgtgttgtg 420

gtagacatca gcaaggatga tcccgaggtc agttcagct ggtttgtaga tgatgtggag 480

gtgcacacag ctcagacgca accccgggag gagcagttca acagcacttt ccgctcagtc 540

agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggta 600

aacagtgcag ctttccctgc ccccatcgag aaaaccatct ccaaaaccaa aggcagaccg 660

aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaagtc 720

agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtgg 780

aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct 840

tacttcgtct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc 900

acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctcccac 960

tctcctggta aa 972

<210> 58

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Human CH3

<400> 58
gaattaagga tccaaagcca aaggccagcc ccgcgaacc 39

<210> 59

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Human CH3

<400> 59
tttattgatt attgctcgag tttacccgga gacaggga 38

<210> 60

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Murine CH3

<400> 60
aattaatgaa ttaaggatcc aagaccaagg gccgcccgaa gg 42

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Murine CH3

<400> 61
tttattgatt attgctcgag cttgcccggg gagtgagaga gg 42

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH3

<400> 62
aattaatgaa ttaaggatcc cgcaccaaag gccctgcc 38

<210> 63

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH3

<400> 63
tttattgatt attgctcgag cttgccggcg gacttggagg 40

<210> 64

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH2CH3

<400> 64
ttaatgaatt aaggatccgg cggcccatct gtgttcatct tc 42

<210> 65

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH2CH3

<400> 65
tttattgatt attgctcgag cttgccggcg gacttggagg 40

<210> 66

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence of IgG Fc sequences

<400> 66

His Cys Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
1 5 10 15

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
20 25 30

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
35 40 45

Gln Pro Val Phe Ser Trp Tyr Val Asp Gly Val Glu Val His Thr Ala
50 55 60

Lys Met Leu Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
65 70 75 80

Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Asn Gly Lys
85 90 95

Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu
100 105 110

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Glu Pro Gln Val
115 120 125

Tyr Val Leu Pro Pro Pro Arg Glu Glu Leu Ser Lys Asn Asp Thr Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile Ala Val
145 150 155 160

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Asn Lys Tyr Lys Thr
165 170 175

Thr Pro Pro Gln Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
180 185 190

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Thr Phe Thr Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
210 215 220

Ser Lys Ser Pro Gly Lys
225 230

<210> 67

<211> 471

<212> PRT

<213> Mouse

<400> 67

Thr Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala
1 5 10 15

Ser Ala Thr Ser Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
20 25 30

Gln Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
35 40 45

Phe Ser Ser Phe Ala Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
50 55 60

Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Ser Ile Thr Ile Tyr Tyr
65 70 75 80

Ala Asp Thr Val Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Pro Lys
85 90 95

Ser Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Ala Arg Asp Asp Tyr Gly Ser Ser Gly Trp Tyr Phe
115 120 125

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr
130 135 140

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
145 150 155 160

Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
165 170 175

Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
195 200 205

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
210 215 220

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
225 230 235 240

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
245 250 255

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
260 265 270

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
275 280 285

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
290 295 300

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
305 310 315 320

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
340 345 350

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
355 360 365

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
370 375 380

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
385 390 395 400

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
405 410 415

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
420 425 430

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
435 440 445

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
450 455 460

Lys Ser Glu Lys Asp Glu Leu
465 470

<210> 68

<211> 244

<212> PRT

<213> Mouse

<400> 68

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
20 25 30

Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
100 105 110

Cys Thr Gln Ser Tyr Asn Leu Leu Thr Phe Gly Ala Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu
225 230 235 240

Lys Asp Glu Leu

<210> 69

<211> 469

<212> PRT

<213> Mouse

<400> 69

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1               5                  10                  15

Ala Thr Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30

Thr Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Asp Tyr Ser Leu
        35                  40                  45

Thr Asp Tyr Tyr Met His Trp Val Lys Gln Ser His Gly Glu Ser Leu
    50                  55                  60

Glu Trp Ile Gly Tyr Ile Asn Phe Tyr Asn Gly Ala Thr Asn Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Phe Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Val Tyr Met Gln Phe Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Val Arg Glu Ala Leu Leu Arg Asn Tyr Ala Met Asp Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro
    130                 135                 140

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
145                 150                 155                 160

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
                165                 170                 175

Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
            180                 185                 190

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
        195                 200                 205

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
    210                 215                 220

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
225                 230                 235                 240

Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
                245                 250                 255
```

Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
260 265 270

Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
275 280 285

Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
290 295 300

Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
305 310 315 320

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
325 330 335

Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
355 360 365

Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
370 375 380

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
385 390 395 400

Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
405 410 415

Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
420 425 430

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
435 440 445

His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ser
450 455 460

Glu Lys Asp Glu Leu
465

<210> 70

<211> 240

<212> PRT

<213> mouse

<400> 70

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
20 25 30

Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
35 40 45

Ser Ser Arg Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro
50 55 60

Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
100 105 110

Gly Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
225 230 235 240

<210> 71

<211> 474

<212> PRT

<213> Mouse

<400> 71

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Met Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
50 55 60

Glu Trp Val Ala Glu Ile Arg Leu Thr Ser Asn Asn Phe Ala Thr His
65 70 75 80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr
100 105 110

Gly Ile Tyr Tyr Cys Thr Arg Pro Tyr Tyr Gly Gly Arg Phe Phe Tyr
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135 140

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
145 150 155 160

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
165 170 175

```
Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
        195                 200                 205

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
    210                 215                 220

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
                245                 250                 255

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
            260                 265                 270

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
        275                 280                 285

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
    290                 295                 300

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
305                 310                 315                 320

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
                325                 330                 335

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
            340                 345                 350

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
        355                 360                 365

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
    370                 375                 380

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
385                 390                 395                 400

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
                405                 410                 415

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
            420                 425                 430
```

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
435 440 445

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
450 455 460

Ser Pro Gly Lys Ser Glu Lys Asp Glu Leu
465 470

<210> 72

<211> 240

<212> PRT

<213> Mouse

<400> 72

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Glu Ile Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
20 25 30

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile
35 40 45

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Val
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
85 90 95

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Asn
100 105 110

Ser Ile Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
225 230 235 240

<210> 73

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 VL

<400> 73

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile
1 5 10

<210> 74

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 VL

<400> 74

Val Arg Leu Thr Gln Ser Pro Ala Ile
1 5

<210> 75

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 VH

<400> 75

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
1 5 10

<210> 76

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 VH

<400> 76

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
1 5 10

<210> 77

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 derived VL produced in Cor
n

<400> 77

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile
1 5 10

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 derived VL produced in Corn

<400> 78

Leu Val Leu Thr Gln Ser Pro Ala Ile
1 5

<210> 79

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 derived VH produced in Cor
n

<400> 79

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
1 5 10

<210> 80

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 derived VH produced in Corn

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X at position 2 denotes that this residue was not obtained during sequencing

<400> 80

Glu Xaa Gln Leu Gln Gln Ser Gly Pro Glu
1 5 10